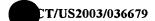SEQUENCE LISTING

<110> Zimmerman, et al.

<120> METHODS FOR PREVENTING AND TREATING CANCER METASTASIS AND BONE LOSS
ASSOCIATED WITH CANCER METASTASIS

<130> 27527/39636A

<150> US 60/426,781
<151> 2002-11-15

<160> 8

<170> PatentIn version 3.2

<210> 1
<211> 1855
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (190)..(960)

<220>
<221> sig_peptide
<222> (190)..(285)

<220>
<221> mat_peptide
<222> (286)..(957)

<400> 1
gagggctggc cagtgaggct cggcccgggg aaagtgaaag tttgcctggg tcctctcggc   60

gccagagccg ctctccgcat cccaggacag cggtgcggcc ctcggccggg gcgcccactc   120

cgcagcagcc agcgagcgag cgagcgagcg agggcggccg acgcgcccgg ccgggaccca   180

gctgcccgt atg acc gcg ccg ggc gcc gcc ggg cgc tgc cct ccc acg aca   231
          Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr
          1   5   10

tgg ctg ggc tcc ctg ctg ttg ttg gtc tgt ctc ctg gcg agc agg agt   279
Trp Leu Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser
15   20   25   30

atc acc gag gag gtg tcg gag tac tgt agc cac atg att ggg agt gga   327
Ile Thr Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly
                35   40   45

cac ctg cag tct ctg cag cgg ctg att gac agt cag atg gag acc tcg   375
His Leu Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser
            50   55   60

tgc caa att aca ttt gag ttt gta gac cag gaa cag ttg aaa gat cca   423
Cys Gln Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro
            65   70   75

gtg tgc tac ctt aag aag gca ttt ctc ctg gta caa gac ata atg gag   471
Val Cys Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu
            80   85   90

```
gac acc atg cgc ttc aga gat aac acc ccc aat gcc atc gcc att gtg     519
Asp Thr Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val
95              100                 105                 110

cag ctg cag gaa ctc tct ttg agg ctg aag agc tgc ttc acc aag gat     567
Gln Leu Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp
            115                 120                 125

tat gaa gag cat gac aag gcc tgc gtc cga act ttc tat gag aca cct     615
Tyr Glu Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro
            130                 135                 140

ctc cag ttg ctg gag aag gtc aag aat gtc ttt aat gaa aca aag aat     663
Leu Gln Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn
        145                 150                 155

ctc ctt gac aag gac tgg aat att ttc agc aag aac tgc aac aac agc     711
Leu Leu Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser
        160                 165                 170

ttt gct gaa tgc tcc agc caa ggc cat gag agg cag tcc gag gga tcc     759
Phe Ala Glu Cys Ser Ser Gln Gly His Glu Arg Gln Ser Glu Gly Ser
175             180                 185                 190

tcc agc ccg cag ctc cag gag tct gtc ttc cac ctg ctg gtg ccc agt     807
Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu Leu Val Pro Ser
            195                 200                 205

gtc atc ctg gtc ttg ctg gcc gtc gga ggc ctc ttg ttc tac agg tgg     855
Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu Phe Tyr Arg Trp
            210                 215                 220

agg cgg cgg agc cat caa gag cct cag aga gcg gat tct ccc ttg gag     903
Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp Ser Pro Leu Glu
        225                 230                 235

caa cca gag ggc agc ccc ctg act cag gat gac aga cag gtg gaa ctg     951
Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg Gln Val Glu Leu
        240                 245                 250

cca gtg tag aggggaattct aagctggacg cacagaacag tctctccgtg            1000
Pro Val
255

ggaggagaca ttatggggcg tccaccacca cccctccctg gccatcctcc tggaatgtgg    1060

tctgccctcc accagagctc ctgcctgcca ggactggacc agagcagcca ggctggggcc    1120

cctctgtctc aacccgcaga cccttgactg aatgagagag gccagaggat gctccccatg    1180

ctgccactat ttattgtgag ccctggaggc tcccatgtgc ttgaggaagg ctggtgagcc    1240

cggctcagga ccctcttccc tcaggggctg caccctcctc tcactccctt ccatgccgga    1300

acccaggcca gggacccacc ggcctgtggt ttgtgggaaa gcagggtgga cgctgaggag    1360

tgaaagaacc ctgcacccag agggcctgcc tggtgccaag gtatcccagc ctggacaggc    1420

atggacctgt ctccagagag aggagcctga agttcgtggg cgggacagc gtcggcctga     1480

tttcccgtaa aggtgtgcag cctgagagac gggaagagga ggcctctgga cctgctggtc    1540

tgcactgaca gcctgaaggg tctacaccct cggctcacct aagtgccctg tgctggttgc    1600
```

```
caggcgcaga  ggggaggcca  gccctgccct  caggacctgc  ctgacctgcc  agtgatgcca   1660

agaggggat   caagcactgg  cctctgcccc  tcctccttcc  agcacctgcc  agagcttctc   1720

caggaggcca  agcagaggct  cccctcatga  aggaagccat  tgcactgtga  acactgtacc   1780

tgcctgctga  acagcctgcc  cccgtccatc  catgagccag  catccgtccg  tcctccactc   1840

tccagcctct  cccca                                                        1855
```

<210> 2
<211> 256
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                   10                  15


Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
            20                  25                  30


Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35                  40                  45


Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50                  55                  60


Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65                  70                  75                  80


Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
                85                  90                  95


Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100                 105                 110


Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115                 120                 125


Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130                 135                 140


Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145                 150                 155                 160


Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
                165                 170                 175
```

```
Glu Cys Ser Ser Gln Gly His Glu Arg Gln Ser Glu Gly Ser Ser Ser
            180                 185                 190

Pro Gln Leu Gln Glu Ser Val Phe His Leu Leu Val Pro Ser Val Ile
        195                 200                 205

Leu Val Leu Leu Ala Val Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg
    210                 215                 220

Arg Ser His Gln Glu Pro Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro
225                 230                 235                 240

Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg Gln Val Glu Leu Pro Val
                245                 250                 255
```

```
<210>  3
<211>  2749
<212>  DNA
<213>  Homo sapiens

<220>
<221>  CDS
<222>  (190)..(1854)

<220>
<221>  sig_peptide
<222>  (190)..(285)

<220>
<221>  mat_peptide
<222>  (286)..(1851)

<400>  3
gagggctggc cagtgaggct cggcccgggg aaagtgaaag tttgcctggg tcctctcggc     60

gccagagccg ctctccgcat cccaggacag cggtgcggcc ctcggccggg gcgcccactc    120

cgcagcagcc agcgagcgag cgagcgagcg agggcggccg acgcgcccgg ccgggaccca    180

gctgcccgt atg acc gcg ccg ggc gcc gcc ggg cgc tgc cct ccc acg aca    231
            Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr
            1               5                   10

tgg ctg ggc tcc ctg ctg ttg ttg gtc tgt ctc ctg gcg agc agg agt    279
Trp Leu Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser
15                  20                  25                  30

atc acc gag gag gtg tcg gag tac tgt agc cac atg att ggg agt gga    327
Ile Thr Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly
                35                  40                  45

cac ctg cag tct ctg cag cgg ctg att gac agt cag atg gag acc tcg    375
His Leu Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser
            50                  55                  60

tgc caa att aca ttt gag ttt gta gac cag gaa cag ttg aaa gat cca    423
Cys Gln Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro
        65                  70                  75
```
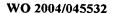
```
gtg tgc tac ctt aag aag gca ttt ctc ctg gta caa gac ata atg gag      471
Val Cys Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu
    80              85                  90

gac acc atg cgc ttc aga gat aac acc ccc aat gcc atc gcc att gtg      519
Asp Thr Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val
95              100                 105                 110

cag ctg cag gaa ctc tct ttg agg ctg aag agc tgc ttc acc aag gat      567
Gln Leu Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp
                115                 120                 125

tat gaa gag cat gac aag gcc tgc gtc cga act ttc tat gag aca cct      615
Tyr Glu Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro
                130                 135                 140

ctc cag ttg ctg gag aag gtc aag aat gtc ttt aat gaa aca aag aat     ·663
Leu Gln Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn
        145                 150                 155

ctc ctt gac aag gac tgg aat att ttc agc aag aac tgc aac aac agc      711
Leu Leu Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser
    160                 165                 170

ttt gct gaa tgc tcc agc caa gat gtg gtg acc aag cct gat tgc aac      759
Phe Ala Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn
175                 180                 185                 190

tgc ctg tac ccc aaa gcc atc cct agc agt gac ccg gcc tct gtc tcc      807
Cys Leu Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser
                195                 200                 205

cct cat cag ccc ctc gcc ccc tcc atg gcc cct gtg gct ggc ttg acc      855
Pro His Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr
                210                 215                 220

tgg gag gac tct gag gga act gag ggc agc tcc ctc ttg cct ggt gag      903
Trp Glu Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu
        225                 230                 235

cag ccc ctg cac aca gtg gat cca ggc agt gcc aag cag cgg cca ccc      951
Gln Pro Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro
    240                 245                 250

agg agc acc tgc cag agc ttt gag ccg cca gag acc cca gtt gtc aag      999
Arg Ser Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys
255                 260                 265                 270

gac agc acc atc ggt ggc tca cca cag cct cgc ccc tct gtc ggg gcc     1047
Asp Ser Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala
                275                 280                 285

ttc aac ccc ggg atg gag gat att ctt gac tct gca atg ggc act aat     1095
Phe Asn Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn
                290                 295                 300

tgg gtc cca gaa gaa gcc tct gga gag gcc agt gag att ccc gta ccc     1143
Trp Val Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro
        305                 310                 315

caa ggg aca gag ctt tcc ccc tcc agg cca gga ggg ggc agc atg cag     1191
Gln Gly Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln
        320                 325                 330
```

```
aca gag ccc gcc aga ccc agc aac ttc ctc tca gca tct tct cca ctc    1239
Thr Glu Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu
335             340             345                     350

cct gca tca gca aag ggc caa cag ccg gca gat gta act ggt aca gcc    1287
Pro Ala Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala
                355.                360                     365

ttg ccc agg gtg ggc ccc gtg agg ccc act ggc cag gac tgg aat cac    1335
Leu Pro Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His
            370             375                 380

acc ccc cag aag aca gac cat cca tct gcc ctg ctc aga gac ccc ccg    1383
Thr Pro Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro
        385             390                 395

gag cca ggc tct ccc agg atc tca tca ctg cgc ccc cag ggc ctc agc    1431
Glu Pro Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Gly Leu Ser
    400             405                 410

aac ccc tcc acc ctc tct gct cag cca cag ctt tcc aga agc cac tcc    1479
Asn Pro Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser
415             420                 425                 430

tcg ggc agc gtg ctg ccc ctt ggg gag ctg gag ggc agg agg agc acc    1527
Ser Gly Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg·Arg Ser Thr
            435             440                 445

agg gat cgg agg agc ccc gca gag cca gaa gga gga cca gca agt gaa    1575
Arg Asp Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu
            450             455                 460

ggg gca gcc agg ccc ctg ccc cgt ttt aac tcc gtt cct ttg act gac    1623
Gly Ala Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp
        465             470                 475

aca ggc cat gag agg cag tcc gag gga tcc tcc agc ccg cag ctc cag    1671
Thr Gly His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln
        480             485                 490

gag tct gtc ttc cac ctg ctg gtg ccc agt gtc atc ctg gtc ttg ctg    1719
Glu Ser Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu
495             500                 505                 510

gcc gtc gga ggc ctc ttg ttc tac agg tgg agg cgg cgg agc cat caa    1767
Ala Val Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln
            515             520                 525

gag cct cag aga gcg gat tct ccc ttg gag caa cca gag ggc agc ccc    1815
Glu Pro Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro
            530             535                 540

ctg act cag gat gac aga cag gtg gaa ctg cca gtg tag agggaattct    1864
Leu Thr Gln Asp Asp Arg Gln Val Glu Leu Pro Val
            545             550

aagctggacg cacagaacag tctctccgtg ggaggagaca ttatggggcg tccaccacca    1924

cccctccctg gccatcctcc tggaatgtgg tctgccctcc accagagctc ctgcctgcca    1984

ggactggacc agagcagcca ggctggggcc cctctgtctc aacccgcaga cccttgactg    2044

aatgagagag gccagaggat gctccccatg ctgccactat ttattgtgag ccctggaggc    2104
```

```
tcccatgtgc ttgaggaagg ctggtgagcc cggctcagga ccctcttccc tcaggggctg   2164

caccctcctc tcactccctt ccatgccgga acccaggcca gggacccacc ggcctgtggt   2224

ttgtgggaaa gcagggtgga cgctgaggag tgaaagaacc ctgcacccag agggcctgcc   2284

tggtgccaag gtatcccagc ctggacaggc atggacctgt ctccagagag aggagcctga   2344

agttcgtggg gcgggacagc gtcggcctga tttcccgtaa aggtgtgcag cctgagagac   2404

gggaagagga ggcctctgga cctgctggtc tgcactgaca gcctgaaggg tctacaccct   2464

cggctcacct aagtgccctg tgctggttgc caggcgcaga ggggaggcca gccctgccct   2524

caggacctgc ctgacctgcc agtgatgcca agagggggat caagcactgg cctctgcccc   2584

tcctccttcc agcacctgcc agagcttctc caggaggcca agcagaggct cccctcatga   2644

aggaagccat tgcactgtga acactgtacc tgcctgctga acagcctgcc cccgtccatc   2704

catgagccag catccgtccg tcctccactc tccagcctct cccca               2749
```

<210> 4
<211> 554
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                   10                  15

Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
                20                  25                  30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
            35                  40                  45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
        50                  55                  60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65                  70                  75                  80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
                85                  90                  95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100                 105                 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115                 120                 125
```
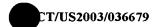
-7-

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130   135   140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145   150   155   160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
            165   170   175

Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
         180   185   190

Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
      195   200   205

Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
    210   215   220

Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225   230   235   240

Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
         245   250   255

Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
         260   265   270

Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
         275   280   285

Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
    290   295   300

Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305   310   315   320

Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
         325   330   335

Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
         340   345   350

Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala Leu Pro
      355   360   365

Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His Thr Pro
370   375   380

```
Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
385             390             395             400


Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Gly Leu Ser Asn Pro
            405             410             415


Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
        420             425             430


Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
        435             440             445


Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala
    450             455             460


Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
465             470             475             480


His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
            485             490             495


Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
        500             505             510


Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
        515             520             525


Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
    530             535             540


Gln Asp Asp Arg Gln Val Glu Leu Pro Val
545             550
```

```
<210>   5
<211>   1519
<212>   DNA
<213>   Homo sapiens

<220>
<221>   CDS
<222>   (190)..(1506)

<220>
<221>   sig_peptide
<222>   (190)..(285)

<220>
<221>   mat_peptide
<222>   (286)..(1503)

<400>   5
gagggctggc cagtgaggct cggcccgggg aaagtgaaag tttgcctggg tcctctcggc        60
```
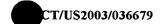
gccagagccg ctctccgcat cccaggacag cggtgcggcc ctcggccggg gcgcccactc   120

cgcagcagcc agcgagcgag cgagcgagcg agggcggccg acgcgcccgg ccgggaccca   180

gctgcccgt atg acc gcg ccg ggc gcc gcc ggg cgc tgc cct ccc acg aca   231
         Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr
          1   5   10

tgg ctg ggc tcc ctg ctg ttg ttg gtc tgt ctc ctg gcg agc agg agt   279
Trp Leu Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser
15   20   25   30

atc acc gag gag gtg tcg gag tac tgt agc cac atg att ggg agt gga   327
Ile Thr Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly
                 35   40   45

cac ctg cag tct ctg cag cgg ctg att gac agt cag atg gag acc tcg   375
His Leu Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser
             50   55   60

tgc caa att aca ttt gag ttt gta gac cag gaa cag ttg aaa gat cca   423
Cys Gln Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro
         65   70   75

gtg tgc tac ctt aag aag gca ttt ctc ctg gta caa gac ata atg gag   471
Val Cys Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu
     80   85   90

gac acc atg cgc ttc aga gat aac acc ccc aat gcc atc gcc att gtg   519
Asp Thr Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val
95   100   105   110

cag ctg cag gaa ctc tct ttg agg ctg aag agc tgc ttc acc aag gat   567
Gln Leu Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp
                 115   120   125

tat gaa gag cat gac aag gcc tgc gtc cga act ttc tat gag aca cct   615
Tyr Glu Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro
             130   135   140

ctc cag ttg ctg gag aag gtc aag aat gtc ttt aat gaa aca aag aat   663
Leu Gln Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn
             145   150   155

ctc ctt gac aag gac tgg aat att ttc agc aag aac tgc aac aac agc   711
Leu Leu Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser
     160   165   170

ttt gct gaa tgc tcc agc caa gat gtg gtg acc aag cct gat tgc aac   759
Phe Ala Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn
175   180   185   190

tgc ctg tac ccc aaa gcc atc cct agc agt gac ccg gcc tct gtc tcc   807
Cys Leu Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser
                 195   200   205

cct cat cag ccc ctc gcc ccc tcc atg gcc cct gtg gct ggc ttg acc   855
Pro His Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr
             210   215   220

tgg gag gac tct gag gga act gag ggc agc tcc ctc ttg cct ggt gag   903
Trp Glu Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu
             225   230   235

- 10 -

```
cag ccc ctg cac aca gtg gat cca ggc agt gcc aag cag cgg cca ccc      951
Gln Pro Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro
    240             245                 250

agg agc acc tgc cag agc ttt gag ccg cca gag acc cca gtt gtc aag      999
Arg Ser Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys
255             260                 265                 270

gac agc acc atc ggt ggc tca cca cag cct cgc ccc tct gtc ggg gcc     1047
Asp Ser Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala
                275                 280                 285

ttc aac ccc ggg atg gag gat att ctt gac tct gca atg ggc act aat     1095
Phe Asn Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn
                290                 295                 300

tgg gtc cca gaa gaa gcc tct gga gag gcc agt gag att ccc gta ccc     1143
Trp Val Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro
            305                 310                 315

caa ggg aca gag ctt tcc ccc tcc agg cca gga ggg ggc agc atg cag     1191
Gln Gly Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln
    320                 325                 330

aca gag ccc gcc aga ccc agc aac ttc ctc tca gca tct tct cca ctc     1239
Thr Glu Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu
335                 340                 345                 350

cct gca tca gca aag ggc caa cag ccg gca gat gta act ggc cat gag     1287
Pro Ala Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly His Glu
                355                 360                 365

agg cag tcc gag gga tcc tcc agc ccg cag ctc cag gag tct gtc ttc     1335
Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe
            370                 375                 380

cac ctg ctg gtg ccc agt gtc atc ctg gtc ttg ctg gcc gtc gga ggc     1383
His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly
            385                 390                 395

ctc ttg ttc tac agg tgg agg cgg cgg agc cat caa gag cct cag aga     1431
Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg
    400                 405                 410

gcg gat tct ccc ttg gag caa cca gag ggc agc ccc ctg act cag gat     1479
Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp
415                 420                 425                 430

gac aga cag gtg gaa ctg cca gtg tag agggaattct aag                  1519
Asp Arg Gln Val Glu Leu Pro Val
                435
```

```
<210>   6
<211>   438
<212>   PRT
<213>   Homo sapiens

<400>   6

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1               5                   10                  15
```
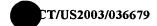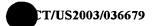
```
Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
        20              25              30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
        35              40              45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
    50              55              60 .

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65              70              75              80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
            85              90              95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
            100             105             110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
        115             120             125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
    130             135             140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145             150             155             160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
            165             170             175

Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
        180             185             190

Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
        195             200             205

Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
    210             215             220

Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225             230             235             240

Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
            245             250             255

Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
            260             265             270
```

- 12 -

Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
        275   280   285 ·

Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
    290   295   300

Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
305   310   315   320

Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
            325   330   335

Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
        340   345   350

Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly His Glu Arg Gln
        355   360   365

Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu
    370   375   380

Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu
385   390   395   400

Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp
            405   410   415

Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg
    .   420   425   430

Gln Val Glu Leu Pro Val
        435

<210> 7
<211> 3985
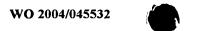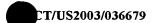<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (293)..(3211)

<220> ·
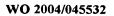<221> sig_peptide
<222> (293)..(349)

<220>
<221> mat_peptide
<222> (350)..(3208)

<220>
<221> misc_feature

```
<222>  (374)..(598)
<223>  Immunoglobulin

<220>
<221>  misc_feature
<222>  (917)..(1177)
<223>  Immunoglobulin

<220>
<221>  misc_feature
<222>  (2516)..(3022)
<223>  Tyrosine Kinase, Catalytic Domain

<400>  7
gaagggcaga cagagtgtcc aaaagcgtga gagcacgaag tgaggagaag gtggagaaga      60

gagaagagga agaggaagag gaagagagga agcggaggga actgcggcca ggctaaaagg     120

ggaagaagag gatcagccca aggaggagga agaggaaaac aagacaaaca gccagtgcag     180

aggagaggaa cgtgtgtcca gtgtcccgat ccctgcggag ctagtagctg agagctctgt     240

gccctgggca ccttgcagcc ctgcacctgc ctgccacttc cccaccgagg cc atg ggc     298
                                                          Met Gly
                                                           1
```

```
cca gga gtt ctg ctg ctc ctg ctg gtg gcc aca gct tgg cat ggt cag      346
Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His Gly Gln
         5                   10                  15

gga atc cca gtg ata gag ccc agt gtc cct gag ctg gtc gtg aag cca      394
Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro
    20                  25                  30

gga gca acg gtg acc ttg cga tgt gtg ggc aat ggc agc gtg gaa tgg      442
Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp
35                  40                  45                  50

gat ggc ccc cca tca cct cac tgg acc ctg tac tct gat ggc tcc agc      490
Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser
                 55                  60                  65

agc atc ctc agc acc aac aac gct acc ttc caa aac acg ggg acc tat      538
Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr
                 70                  75                  80

cgc tgc act gag cct gga gac ccc ctg gga ggc agc gcc gcc atc cac      586
Arg Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His
        85                  90                  95

ctc tat gtc aaa gac cct gcc cgg ccc tgg aac gtg cta gca cag gag      634
Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu
    100                 105                 110

gtg gtc gtg ttc gag gac cag gac gca cta ctg ccc tgt ctg ctc aca      682
Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr
115                 120                 125                 130

gac ccg gtg ctg gaa gca ggc gtc tcg ctg gtg cgt gtg cgt ggc cgg      730
Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg Gly Arg
                 135                 140                 145
```

- 14 -

```
ccc ctc atg cgc cac acc aac tac tcc ttc tcg ccc tgg cat ggc ttc      778
Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe
            150             155             160

acc atc cac agg gcc aag ttc att cag agc cag gac tat caa tgc agt      826
Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser
            165             170             175

gcc ctg atg ggt ggc agg aag gtg atg tcc atc agc atc cgg ctg aaa      874
Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys
    180             185             190

gtg cag aaa gtc atc cca ggg ccc cca gcc ttg aca ctg gtg cct gca      922
Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala
195             200             205             210

gag ctg gtg cgg att cga ggg gag gct gcc cag atc gtg tgc tca gcc      970
Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala
            215             220             225

agc agc gtt gat gtt aac ttt gat gtc ttc ctc caa cac aac aac acc     1018
Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr
            230             235             240

aag ctc gca atc cct caa caa tct gac ttt cat aat aac cgt tac caa     1066
Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln
            245             250             255

aaa gtc ctg acc ctc aac ctc gat caa gta gat ttc caa cat gcc ggc     1114
Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly
    260             265             270

aac tac tcc tgc gtg gcc agc aac gtg cag ggc aag cac tcc acc tcc     1162
Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser
275             280             285             290

atg ttc ttc cgg gtg gta gag agt gcc tac ttg aac ttg agc tct gag     1210
Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu
            295             300             305

cag aac ctc atc cag gag gtg acc gtg ggg gag ggg ctc aac ctc aaa     1258
Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn Leu Lys
            310             315             320

gtc atg gtg gag gcc tac cca ggc ctg caa ggt ttt aac tgg acc tac     1306
Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp Thr Tyr
            325             330             335

ctg gga ccc ttt tct gac cac cag cct gag ccc aag ctt gct aat gct     1354
Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala Asn Ala
    340             345             350

acc acc aag gac aca tac agg cac acc ttc acc ctc tct ctg ccc cgc     1402
Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu Pro Arg
355             360             365             370

ctg aag ccc tct gag gct ggc cgc tac tcc ttc ctg gcc aga aac cca     1450
Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg Asn Pro
            375             380             385

gga ggc tgg aga gct ctg acg ttt gag ctc acc ctt cga tac ccc cca     1498
Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr Pro Pro
            390             395             400
```

```
gag gta agc gtc ata tgg aca ttc atc aac ggc tct ggc acc ctt ttg     1546
Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr Leu Leu
        405             410                 415

tgt gct gcc tct ggg tac ccc cag ccc aac gtg aca tgg ctg cag tgc     1594
Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu Gln Cys
        420             425                 430

agt ggc cac act gat agg tgt gat gag gcc caa gtg ctg cag gtc tgg     1642
Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln Val Trp
435             440                 445                 450

gat gac cca tac cct gag gtc ctg agc cag gag ccc ttc cac aag gtg     1690
Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His Lys Val
            455                 460                 465

acg gtg cag agc ctg ctg act gtt gag acc tta gag cac aac caa acc     1738
Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn Gln Thr
            470                 475                 480

tac gag tgc agg gcc cac aac agc gtg ggg agt ggc tcc tgg gcc ttc     1786
Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp Ala Phe
        485                 490                 495

ata ccc atc tct gca gga gcc cac acg cat ccc ccg gat gag ttc ctc     1834
Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu Phe Leu
        500                 505                 510

ttc aca cca gtg gtg gtc gcc tgc atg tcc atc atg gcc ttg ctg ctg     1882
Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu Leu Leu
515                 520                 525                 530

ctg ctg ctc ctg ctg cta ttg tac aag tat aag cag aag ccc aag tac     1930
Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro Lys Tyr
                535                 540                 545

cag gtc cgc tgg aag atc atc gag agc tat gag ggc aac agt tat act     1978
Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser Tyr Thr
        550                 555                 560

ttc atc gac ccc acg cag ctg cct tac aac gag aag tgg gag ttc ccc     2026
Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu Phe Pro
        565                 570                 575

cgg aac aac ctg cag ttt ggt aag acc ctc gga gct gga gcc ttt ggg     2074
Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala Phe Gly
        580                 585                 590

aag gtg gtg gag gcc acg gcc ttt ggt ctg ggc aag gag gat gct gtc     2122
Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp Ala Val
595                 600                 605                 610

ctg aag gtg gct gtg aag atg ctg aag tcc acg gcc cat gct gat gag     2170
Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala Asp Glu
            615                 620                 625

aag gag gcc ctc atg tcc gag ctg aag atc atg agc cac ctg ggc cag     2218
Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu Gly Gln
            630                 635                 640

cac gag aac atc gtc aac ctt ctg gga gcc tgt acc cat gga ggc cct     2266
His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly Gly Pro
        645                 650                 655
```

```
gta ctg gtc atc acg gag tac tgt tgc tat ggc gac ctg ctc aac ttt    2314
Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Phe
    660             665             670

ctg cga agg aag gct gag gcc atg ctg gga ccc agc ctg agc ccc ggc    2362
Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser Pro Gly
675             680             685             690

cag gac ccc gag gga ggc gtc gac tat aag aac atc cac ctc gag aag    2410
Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu Glu Lys
            695             700             705

aaa tat gtc cgc agg gac agt ggc ttc tcc agc cag ggt gtg gac acc    2458
Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val Asp Thr
        710             715             720

tat gtg gag atg agg cct gtc tcc act tct tca aat gac tcc ttc tct    2506
Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser Phe Ser
        725             730             735

gag caa gac ctg gac aag gag gat gga cgg ccc ctg gag ctc cgg gac    2554
Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu Arg Asp
    740             745             750

ctg ctt cac ttc tcc agc caa gta gcc cag ggc atg gcc ttc ctc gct    2602
Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe Leu Ala
755             760             765             770

tcc aag aat tgc atc cac cgg gac gtg gca gcg cgt aac gtg ctg ttg    2650
Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val Leu Leu
            775             780             785

acc aat ggt cat gtg gcc aag att ggg gac ttc ggg ctg gct agg gac    2698
Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala Arg Asp
            790             795             800

atc atg aat gac tcc aac tac att gtc aag ggc aat gcc cgc ctg cct    2746
Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg Leu Pro
        805             810             815

gtg aag tgg atg gcc cca gag agc atc ttt gac tgt gtc tac acg gtt    2794
Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr Thr Val
    820             825             830

cag agc gac gtc tgg tcc tat ggc atc ctc ctc tgg gag atc ttc tca    2842
Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser
835             840             845             850

ctt ggg ctg aat ccc tac cct ggc atc ctg gtg aac agc aag ttc tat    2890
Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys Phe Tyr
            855             860             865

aaa ctg gtg aag gat gga tac caa atg gcc cag cct gca ttt gcc cca    2938
Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe Ala Pro
            870             875             880

aag aat ata tac agc atc atg cag gcc tgc tgg gcc ttg gag ccc acc    2986
Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu Pro Thr
            885             890             895

cac aga ccc acc ttc cag cag atc tgc tcc ttc ctt cag gag cag gcc    3034
His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu Gln Ala
    900             905             910
```

```
caa gag gac agg aga gag cgg gac tat acc aat ctg ccg agc agc agc    3082
Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser Ser Ser
915             920             925             930

aga agc ggt ggc agc ggc agc agc agc agt gag ctg gag gag gag agc    3130
Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu Glu Ser
            935             940             945

tct agt gag cac ctg acc tgc tgc gag caa ggg gat atc gcc cag ccc    3178
Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala Gln Pro
        950             955             960

ttg ctg cag ccc aac aac tat cag ttc tgc tga ggagttgacg acagggagta  3231
Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
        965             970
```

ccactctccc ctcctccaaa cttcaactcc tccatggatg gggcgacacg gggagaacat   3291

acaaactctg ccttcggtca tttcactcaa cagctcggcc cagctctgaa acttgggaag   3351

gtgagggatt caggggaggt cagaggatcc cacttcctga gcatgggcca tcactgccag   3411

tcaggggctg ggggctgagc cctcaccccc ccctccccta ctgttctcat ggtgttggcc   3471

tcgtgtttgc tatgccaact agtagaacct tctttcctaa tccccttatc ttcatggaaa   3531

tggactgact ttatgcctat gaagtcccca ggagctacac tgatactgag aaaaccaggc   3591

tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga   3651

tgctcacaga ccacactcag ctcaggcccc ttggagcagg atggctcctc taagaatctc   3711

acaggacctc ttagtctctg ccctatacgc cgccttcact ccacagcctc acccctccca   3771

cccccatact ggtactgctg taatgagcca agtggcagct aaaagttggg ggtgttctgc   3831

ccagtcccgt cattctgggc tagaaggcag gggaccttgg catgtggctg ccacaccaa   3891

gcaggaagca caaactcccc caagctgact catcctaact aacagtcacg ccgtgggatg   3951

tctctgtcca cattaaacta acagcattaa tgca   3985

```
<210>  8
<211>  972
<212>  PRT
<213>  Homo sapiens

<400>  8

Met Gly Pro Gly Val Leu Leu Leu Leu Val Ala Thr Ala Trp His His
1               5                   10                  15


Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
            20              25              30


Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
        35              40              45
```

```
Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
    50              55                  60

Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly
65              70                  75                  80

Thr Tyr Arg Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala
              85              90                  95

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
              100             105             110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
          115             120             125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
    130             135             140

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145             150             155             160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
              165             170             175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
          180             185             190

Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
    195             200             205

Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
    210             215             220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225             230             235             240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
          245             250             255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
          260             265             270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
          275             280             285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
    290             295             300
```

```
Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305               310               315               320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
              325               330               335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
          340               345               350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
          355               360               365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
    370               375               380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385               390               395               400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
              405               410               415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
          420               425               430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
          435               440               445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
    450               455               460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465               470               475               480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
          485               490               495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
          500               505               510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
          515               520               525

Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
    530               535               540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
545               550               555               560
```
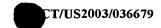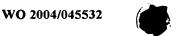
```
Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
                565             570                 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
            580             585                 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
        595             600             605

Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
    610             615             620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625             630             635             640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
            645             650             655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
        660             665             670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
        675             680             685

Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
    690             695             700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705             710             715             720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
            725             730             735

Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
            740             745             750

Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
        755             760             765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
    770             775             780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785             790             795             800

Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
            805             810             815
```

- 21 -

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
            820   825   830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
            835   840   845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
    850   855   860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865   870   875   880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
            885   890   895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
            900   905   910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
    915   920   925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
    930   935   940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945   950   955   960

Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
            965   970